

Package ‘relsurv’

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Description Various functions for relative survival analysis.

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checktimes	<i>Summary of a cumulative incidence curve</i>
------------	--

Description

Returns a list containing the estimated values at required times.

Usage

checktimes(w, times, xscale = 1,area=FALSE)

Arguments

- w output of the function cmp.rel.
- times the times at which the output is required.
- xscale The time scale in which the times are specified. The default value is 1, i.e. days.
- area Should area under the curves at time tau be printed out? Default is FALSE.

Details

The variance is calculated using numerical integration. If the required time is not a time at which the value was estimated, the value at the last time before it is reported. The density of the time points is set by the precision argument in the cmp.rel function.

Value

A list of values is returned.

See Also

cmp.rel

Examples

```
data(slopop)
data(rdata)
#calculate the cumulative incidence curve
#note that the variable year is given in days since 01.01.1960 and that
#age must be multiplied by 365 in order to be expressed in days.
fit <- cmp.rel(Surv(time,cens)~sex+ratetable(age=age*365,sex=sex,
      year=year),ratetable=slopop,data=rdata,tau=3652.41)
checktimes(fit,c(1,3),xscale=365.241)
```

 cmp.rel

Compute crude mortality curves

Description

Estimates the probability of dying due to disease and due to population reasons

Usage

```
cmp.rel(formula, data, ratetable = relsurv::slopop, na.action, tau,
  conf.int=0.95,precision=1,add.times)
```

Arguments

formula	a formula object, with the response as a Surv object on the left of a ~ operator, and, if desired, terms separated by the + operator on the right. If the variables are not organized and named in the same way as in the population tables, a ratetable term must be added to match each subject to his/her expected cohort. For a single survival curve the ~ 1 part of the formula is not required. NOTE: The time must be in days, and the same is required for the ratetable variables (the variables used in the population tables), for example age and year (year must be given in the date format, i.e. in number of days since 01.01.1960).
data	a data.frame in which to interpret the variables named in the formula.
ratetable	a table of event rates, organized as a ratetable object, such as slopop.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
tau	the maximum follow-up time of interest, all times larger than tau shall be censored. Equals maximum observed time by default
conf.int	the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.
precision	the level of precision used in the numerical integration of variance. Default is 1, which means that daily intervals are taken, the value may be decreased to get a higher precision or increased to achieve a faster calculation. The calculation intervals always include at least all times of event and censoring as border points.
add.times	specific times at which the value of estimator and its variance should be evaluated. Default is all the event and censoring times.

Details

NOTE: All times used in the formula argument must be specified in days. This is true for the follow-up time as well as for any variables needed ratetable object, like age and year.

Note that numerical integration is required to calculate the variance estimator. The integration precision is set with argument precision, which defaults to daily intervals, a default that should give enough precision for any practical purpose.

The area under the curve is calculated on the interval $[0, \tau]$.

Function timepoints may be used to get the output at specific points in time.

Value

An object of class `cmp.rel`. Objects of this class have methods for the functions `print` and `plot`. An object of class `cmp.rel` is composed of several lists, each pertaining the cumulative hazard function for one risk and one strata. Each of the lists contains the following objects:

<code>time</code>	the time-points at which the curves are estimated
<code>est</code>	the estimate
<code>var</code>	the variance of the estimate
<code>lower</code>	the lower limit of the confidence interval
<code>upper</code>	the upper limit of the confidence interval
<code>area</code>	the area under the curve calculated on the interval $[0, \tau]$
<code>index</code>	indicator of event and censoring times among all the times in the output. The times added via parameter <code>add.times</code> are also included
<code>add.times</code>	the times added via parameter <code>add.times</code>

See Also

`rs.surv`, `checktimes`

Examples

```
data(slopop)
data(rdata)
#calculate the cumulative incidence curve
#note that the variable year is given in days since 01.01.1960 and that
#age must be multiplied by 365 in order to be expressed in days.
fit <- cmp.rel(Surv(time,cens)~sex+ratetable(age=age*365,sex=sex,
      year=year),ratetable=slopop,data=rdata,tau=3652.41)
fit
plot(fit,col=c(1,1,2,2),xscale=365.241,xlab="Time (years)")
```

colrec*Relative Survival Data*

Description

Survival of patients with colon and rectal cancer diagnosed in 1994-2000.

Usage

```
data(colrec)
```

Format

A data frame with 5971 observations on the following 7 variables:

sex sex (1=male, 2=female).

age age (in days).

diag date of diagnosis (in date format).

time survival time (in days).

stat censoring indicator (0=censoring, 1=death).

stage cancer stage. Values 1-3, code 99 stands for unknown.

site cancer site.

References

Provided by Slovene Cancer Registry. The age, time and diag variables are randomly perturbed to make the identification of patients impossible.

epa*Excess hazard function smoothing*

Description

An Epanechnikov kernel function based smoother for smoothing the baseline excess hazard calculated by the `rsadd` function with the EM method.

Usage

```
epa(fit,bwin,times,n.bwin=16,left=FALSE)
```

Arguments

<code>fit</code>	Fit from the additive relative survival model using the EM method.
<code>bwin</code>	The relative width of the smoothing window (default is 1).
<code>times</code>	The times at which the smoother is to be evaluated. If missing, it is evaluated at all event times.
<code>n.bwin</code>	Number of times that the window width may change.
<code>left</code>	If FALSE (default) smoothing is performed symmetrically, if TRUE only leftside neighbours are considered.

Details

The function performs Epanechnikov kernel smoothing. The follow up time is divided (according to percentiles of event times) into several intervals (number of intervals defined by `n.bwin`) in which the width is calculated as a factor of the maximum span between event times. Boundary effects are also taken into account on both sides.

Value

A list with two components:

<code>lambda</code>	the smoothed excess baseline hazard function
<code>times</code>	the times at which the smoothed excess baseline hazard is evaluated.

References

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741–1749.

EM algorithm: Pohar Perme M., Henderson R., Stare, J. (2009) "An approach to estimation in relative survival regression." *Biostatistics*, **10**: 136–146.

See Also

[rsadd](#),

Examples

```
data(slopop)
data(rdata)
#fit an additive model with the EM method
fit <- rsadd(Surv(time,cens)~sex+age+ratetable(age=age*365.241,
sex=sex,year=year), ratetable=slopop,data=rdata,int=5,method="EM")
sm <- epa(fit)
plot(sm$times,sm$lambda)
```

invtime	<i>Inverse transforming of time in Relative Survival</i>
---------	--

Description

This function can be used when predicting in Relative Survival using the transformed time regression model (using `rstrans` function). It inverses the time from Y to T in relative survival using the given `ratetable`. The times Y can be produced with the `rstrans` function, in which case, this is the reverse function. This function does the transformation for one person at a time.

Usage

```
invtime(y, age, sex, year, scale, ratetable, lower, upper)
```

Arguments

y	time in Y.
age	age of the individual. Must be in days.
sex	sex of the individual. Must be coded in the same way as in the <code>ratetable</code> .
year	date of diagnosis. Must be in date format
scale	numeric value to scale the results. If <code>ratetable</code> is in units/day, <code>scale = 365.241</code> causes the output to be reported in years.
ratetable	a table of event rates, such as <code>survexp.us</code> .
lower	the lower bound of interval where the result is expected. This argument is optional, but, if given, can shorten the time the function needs to calculate the result.
upper	the upper bound of interval where the result is expected. See <code>lower</code>

Details

Works only with `ratetables` that are split by age, sex and year. Transforming can be computationally intensive, use `lower` and/or `upper` to guess the interval of the result and thus speed up the function.

Value

A list of values	
T	the original time
Y	the transformed time

References

Package: Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272-278.

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741-1749.

See Also[rstrans](#)**Examples**

```
data(slopop)
invtime(y = 0.1, age = 23011, sex = 1, year = 9497, ratetable = slopop)
```

joinrate

Join ratetables

Description

The function joins two or more objects organized as `ratetable` by adding a new dimension.

Usage

```
joinrate(tables, dim.name="country")
```

Arguments

<code>tables</code>	a list of <code>ratetables</code> . If names are given, they are included as <code>dimnames</code> .
<code>dim.name</code>	the name of the added dimension.

Details

This function joins two or more `ratetable` objects by adding a new dimension. The cutpoints of all the rate tables are compared and only the common intervals kept. If the intervals defined by the cutpoints are not of the same length, a warning message is displayed. Each rate table must have 3 dimensions, i.e. age, sex and year (the order is not important).

Value

An object of class `ratetable`.

References

Package: Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272-278.

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741-1749.

See Also

[ratetable](#), [transrate.hld](#), [transrate.hmd](#), [transrate](#).

Examples

```
#newpop <- joinrate(list(Arizona=survexp.az,Florida=survexp.fl,
#                          Minnesota=survexp.mn),dim.name="state")
```

nessie

Net Expected Sample Size Is Estimated

Description

Calculates how the sample size decreases in time due to population mortality

Usage

```
nessie(formula, data, ratetable = relsurv::slopop,times)
```

Arguments

formula	a formula object, same as in <code>rs.surv</code> . The right-hand side of the formula object includes the variable that defines the subgroups (a variable of type factor) by which the expected sample size is to be calculated and, if required, the <code>ratetable</code> argument as in all the other functions of the package.
data	a data.frame in which to interpret the variables named in the formula.
ratetable	a table of event rates, organized as a <code>ratetable</code> object, such as <code>slopop</code> .
times	Times at which the calculation should be evaluated - in years!

Details

The function calculates the sample size we can expect at a certain time point if the patients die only due to population causes (population survival * initial sample size in a certain category), i.e. the number of individuals that remains at risk at given timepoints after the individuals who die due to population causes are removed. The result should be used as a guideline for the sensible length of follow-up interval when calculating the net survival.

The first column of the output reports the number of individuals at time 0. The last column of the output reports the conditional expected (population) survival time for each subgroup.

Value

A list of values.

See Also

`rs.surv`

Examples

```
data(slopop)
data(rdata)
rdata$agegr <-cut(rdata$age,seq(40,95,by=5))
nessie(Surv(time,cens)~agegr+ratetable(age=age*365.241,sex=sex,year=year),
ratetable=slopop,data=rdata,times=c(1,3,5,10,15))
```

plot.cmp.rel

Plot the cumulative incidence curves

Description

Plot method for cmp.rel. Plots the probability of dying due to disease and due to population reasons

Usage

```
## S3 method for class 'cmp.rel'
plot(x, main, curvlab, ylim=c(0, 1), xlim, wh=2, xlab="Time (days)",
     ylab="Probability", lty=1:length(x), xscale=1,col=1, lwd=par('lwd'),
     curves, conf.int, all.times=FALSE,...)
```

Arguments

x	a list, with each component representing one curve in the plot, output of the function cmp.rel.
main	the main title for the plot.
curvlab	Curve labels for the plot. Default is names(x), or if that is missing, 1:nc, where nc is the number of curves in x.
ylim	yaxis limits for plot.
xlim	xaxis limits for plot (default is 0 to the largest time in any of the curves).
wh	if a vector of length 2, then the upper right coordinates of the legend; otherwise the legend is placed in the upper right corner of the plot.
xlab	X axis label.
ylab	y axis label.
lty	vector of line types. Default 1:nc (nc is the number of curves in x). For color displays, lty=1, color=1:nc, might be more appropriate. If length(lty)<nc, then lty[1] is used for all.
xscale	Scale of the X axis. Default is in days (1).
col	vector of colors. If length(col)<nc, then the col[1] is used for all.
lwd	vector of line widths. If length(lwd)<nc, then lwd[1] is used for all.
curves	Vector of integers, specifies which curves should be plotted. May take values 1:nc, where nc is the number of curves in x. By default, all of the curves are plotted.

<code>conf.int</code>	Vector of integers, specifies which confidence intervals should be plotted. May take values <code>1:nc</code> , where <code>nc</code> is the number of curves in <code>x</code> . By default, no confidence intervals are plotted.
<code>all.times</code>	By default, the disease specific mortality estimate is plotted as a step function between event or censoring times. If set to <code>TRUE</code> , the graph is evaluated at all estimated times.
<code>...</code>	additional arguments passed to the initial call of the plot function.

Details

By default, the graph is plotted as a step function for the cause specific mortality and as a piecewise linear function for the population mortality. It is evaluated at all event and censoring times even though it constantly changes also between these time points.

If the argument `all.times` is set to `TRUE`, the plot is evaluated at all times that were used for numerical integration in the `cmp.rel` function (there, the default is set to daily intervals). If only specific time points are to be added, this should be done via argument `add.times` in `cmp.rel`.

Value

No value is returned.

See Also

`rs.surv`

Examples

```
data(slopop)
data(rdata)
#calculate the cumulative incidence curve
#note that the variable year is given in days since 01.01.1960 and that
#age must be multiplied by 365.241 in order to be expressed in days.
fit <- cmp.rel(Surv(time,cens)~sex+ratetable(age=age*365.241,sex=sex,
      year=year),ratetable=slopop,data=rdata,tau=3652.41)
plot(fit,col=c(1,1,2,2),xscale=365.241,conf.int=c(1,3))
```

<code>plot.rs.zph</code>	<i>Graphical Inspection of Proportional Hazards Assumption in Relative Survival Models</i>
--------------------------	--

Description

Displays a graph of the scaled partial residuals, along with a smooth curve.

Usage

```
## S3 method for class 'rs.zph'
plot(x, resid=TRUE, df = 4, nsmo = 40,var,cex=1,add=FALSE,col=1,
      lty=1,xlab,ylab,scale=1,...)
```

Arguments

<code>x</code>	result of the <code>rs.zph</code> function.
<code>resid</code>	a logical value, if TRUE the residuals are included on the plot, as well as the smooth fit.
<code>df</code>	the degrees of freedom for the fitted natural spline, <code>df=2</code> leads to a linear fit.
<code>nsmo</code>	number of points used to plot the fitted spline.
<code>var</code>	the set of variables for which plots are desired. By default, plots are produced in turn for each variable of a model. Selection of a single variable allows other features to be added to the plot, e.g., a horizontal line at zero or a main title.
<code>cex</code>	a numerical value giving the amount by which plotting text and symbols should be scaled relative to the default.
<code>add</code>	logical, if TRUE the plot is added to an existing plot
<code>col</code>	a specification for the default plotting color.
<code>lty</code>	the line type.
<code>xlab</code>	x axis label.
<code>ylab</code>	y axis label.
<code>scale</code>	units for x axis, default is 1, i.e. days.
<code>...</code>	Additional arguments passed to the plot function.

References

Goodness of fit: Stare J., Pohar Perme M., Henderson R. (2005) "Goodness of fit of relative survival models." *Statistics in Medicine*, **24**: 3911-3925.

Package: Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272-278.

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741-1749, 2007.

See Also

[rs.zph](#), [plot.cox.zph](#).

Examples

```
data(slopop)
data(rdata)
fit <- rsadd(Surv(time,cens)~sex+as.factor(agegr)+ratetable(age=age*365.241,
                  sex=sex,year=year),ratetable=slopop,data=rdata,int=5)
rszph <- rs.zph(fit)
plot(rszph)
```

rdata	<i>Survival Data</i>
-------	----------------------

Description

Survival data.

Usage

```
data(rdata)
```

Format

A data frame with 1040 observations on the following 6 variables:

time survival time (in days).

cens censoring indicator (0=censoring, 1=death).

age age (in years).

sex sex (1=male, 2=female).

year date of diagnosis (in date format).

agegr age group.

References

Pohar M., Stare J. (2006) "Relative survival analysis in R." Computer Methods and Programs in Biomedicine, **81**: 272-278.

residuals.rsadd	<i>Calculate Residuals for a "rsadd" Fit</i>
-----------------	--

Description

Calculates partial residuals for an additive relative survival model.

Usage

```
## S3 method for class 'rsadd'  
residuals(object, type="schoenfeld", ...)
```

Arguments

object	an object inheriting from class <code>rsadd</code> , representing a fitted additive relative survival model. Typically this is the output from the <code>rsadd</code> function.
type	character string indicating the type of residual desired. Currently only Schoenfeld residuals are implemented.
...	other arguments.

Value

A list of the following values is returned:

res	a matrix containing the residuals for each variable.
varr	the variance for each residual
varr1	the sum of varr.
kvarr	the derivative of each residual, to be used in rs.zph function.
kvarr1	the sum of kvarr.

References

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." Computer Methods and Programs in Biomedicine, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." Computers in biology and medicine, **37**: 1741–1749.

Goodness of fit: Stare J., Pohar Perme M., Henderson R. (2005) "Goodness of fit of relative survival models." Statistics in Medicine, **24**: 3911–3925.

See Also

[rsadd](#).

Examples

```
data(slopop)
data(rdata)
fit <- rsadd(Surv(time,cens)~sex+ratetable(age=age*365.241,sex=sex,year=year),
             ratetable=slopop,data=rdata,int=5)
sresid <- residuals.rsadd(fit)
```

rs.br	<i>Test the Proportional Hazards Assumption for Relative Survival Regression Models</i>
-------	---

Description

Test the proportional hazards assumption for relative survival models (rsadd, rsmul or rstrans) by forming a Brownian Bridge.

Usage

```
rs.br(fit,sc,rho=0,test="max",global=TRUE)
```

Arguments

<code>fit</code>	the result of fitting a relative survival model, using the <code>rsadd</code> , <code>rsmul</code> or <code>rstrans</code> function.
<code>sc</code>	partial residuals calculated by the <code>resid</code> function. This is used to save time if several tests are to be calculated on these residuals and can otherwise be omitted.
<code>rho</code>	a number controlling the weights of residuals. The weights are the number of individuals at risk at each event time to the power ρ . The default is $\rho=0$, which sets all weights to 1.
<code>test</code>	a character string specifying the test to be performed on Brownian bridge. Possible values are "max" (default), which tests the maximum absolute value of the bridge, and <code>cvm</code> , which calculates the Cramer Von Mises statistic.
<code>global</code>	should a global Brownian bridge test be performed, in addition to the per-variable tests

Value

an object of class `rs.br`. This function would usually be followed by both a print and a plot of the result. The plot gives a Brownian bridge for each of the variables. The horizontal lines are the 95 of the Brownian bridge

References

Goodness of fit: Stare J., Pohar Perme M., Henderson R. (2005) "Goodness of fit of relative survival models." *Statistics in Medicine*, **24**: 3911–3925.

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741–1749.

See Also

[rsadd](#), [rsmul](#), [rstrans](#), [resid](#).

Examples

```
data(slopop)
data(rdata)
fit <- rsadd(Surv(time,cens)~sex+ratetable(age=age*365.241,sex=sex,
      year=year),ratetable=slopop,data=rdata,int=5)
rsbr <- rs.br(fit)
rsbr
plot(rsbr)
```

rs.diff

*Test Net Survival Curve Differences***Description**

Tests if there is a difference between two or more net survival curves using a log-rank type test.

Usage

```
rs.diff(formula, data, ratetable = relsurv::slopop, na.action, precision=1)
```

Arguments

formula	a formula object, with the response as a Surv object on the left of a ~ operator, and, if desired, terms separated by the + operator on the right. If the variables are not organized and named in the same way as in the population tables, a ratetable term must be added to match each subject to his/her expected cohort. A formula expression as for other survival models, of the form Surv(time, status) ~ predictors. Each combination of predictor values defines a subgroup. A strata term may be used to produce a stratified test. NOTE: The time must be in days, and the same is required for the ratetable variables (the variables used in the population tables), for example age and year (year must be given in the date format, i.e. in number of days since 01.01.1960).
data	a data.frame in which to interpret the variables named in the formula.
ratetable	a table of event rates, organized as a ratetable object, such as slopop.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
precision	Precision for numerical integration. Default is 1, which means that daily intervals are taken, the value may be decreased to get a higher precision or increased to achieve a faster calculation. The calculation intervals always include at least all times of event and censoring as border points.

Details

NOTE: All times used in the formula argument must be specified in days. This is true for the follow-up time as well as for any variables needed ratetable object, like age and year.

Value

a rsdiff object; can be printed with print.

References

Package: Pohar M., Stare J. (2006) "Relative survival analysis in R." Computer Methods and Programs in Biomedicine, **81**: 272–278

Log-rank type test: Graffeo, N., Castell, F., Belot, A. and Giorgi, R. (2016) "A log-rank-type test to compare net survival distributions. Biometrics. doi: 10.1111/biom.12477"

See Also

rs.surv, survdiff

Examples

```
data(slopop)
data(rdata)
#calculate the relative survival curve
#note that the variable year is given in days since 01.01.1960 and that
#age must be multiplied by 365.241 in order to be expressed in days.
rs.diff(Surv(time,cens)~sex+ratetable(age=age*365.241,sex=sex,
year=year),ratetable=slopop,data=rdata)
```

rs.surv

Compute a Relative Survival Curve

Description

Computes an estimate of the relative survival curve using the Ederer I, Ederer II method, Pohar-Perme method or the Hakulinen method

Usage

```
rs.surv(formula, data,ratetable=relsurv::slopop,na.action,fin.date,
method="pohar-perme", conf.type="log",conf.int=0.95,type="kaplan-meier",
add.times,precision=1)
```

Arguments

formula	a formula object, with the response as a Surv object on the left of a ~ operator, and, if desired, terms separated by the + operator on the right. If the variables are not organized and named in the same way as in the population tables, a ratetable term must be added to match each subject to his/her expected cohort. For a single survival curve the ~ 1 part of the formula is not required. NOTE: The time must be in days, and the same is required for the ratetable variables (the variables used in the population tables), for example age and year (year must be given in the date format, i.e. in number of days since 01.01.1960).
data	a data.frame in which to interpret the variables named in the formula.
ratetable	a table of event rates, organized as a ratetable object, such as slopop.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
fin.date	the date of the study ending, used for calculating the potential follow-up times in the Hakulinen method. If missing, it is calculated as max(year+time).
method	the method for calculating the relative survival. The options are pohar-perme(default), ederer1, ederer2 and hakulinen.

<code>conf.type</code>	one of <code>plain</code> , <code>log</code> (the default), or <code>log-log</code> . The first option causes the standard intervals curve $\pm k \cdot \text{se}(\text{curve})$, where k is determined from <code>conf.int</code> . The <code>log</code> option calculates intervals based on the cumulative hazard or $\log(\text{survival})$. The last option bases intervals on the log hazard or $\log(-\log(\text{survival}))$.
<code>conf.int</code>	the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.
<code>type</code>	defines how survival estimates are to be calculated given the hazards. The default (<code>kaplan-meier</code>) calculates the product integral, whereas the option <code>fleming-harrington</code> exponentiates the negative cumulative hazard. Analogous to the usage in <code>survfit</code> .
<code>add.times</code>	specific times at which the curve should be evaluated.
<code>precision</code>	Precision for numerical integration. Default is 1, which means that daily intervals are taken, the value may be decreased to get a higher precision or increased to achieve a faster calculation. The calculation intervals always include at least all times of event and censoring as border points.

Details

NOTE: All times used in the formula argument must be specified in days. This is true for the follow-up time as well as for any variables needed `ratetable` object, like `age` and `year`.

The potential censoring times needed for the calculation of the expected survival by the Hakulinen method are calculated automatically. The times of censoring are left as they are, the times of events are replaced with `fin.date - year`.

The calculation of the Pohar-Perme estimate is more time consuming since more data are needed from the population tables. The old version of the function, now named `rs.survo` can be used as a faster version for the Hakulinen and Ederer II estimate.

Numerical integration is required for Pohar-Perme estimate. The integration precision is set with argument `precision`, which defaults to daily intervals, a default that should give enough precision for any practical purpose.

Note that even though the estimate is always calculated using numerical integration, only the values at event and censoring times are reported. Hence, the function `plot` draws a step function in between and the function `summary` reports the value at the last event or censoring time before the specified time. If the output of the estimated values at other points is required, this should be specified with argument `add.times`.

Value

a `survfit` object; see the help on `survfit.object` for details. The `survfit` methods are used for `print`, `summary`, `plot`, `lines`, and `points`.

References

- Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272–278
- Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741–1749.

See Also

survfit, survexp

Examples

```
data(slopop)
data(rdata)
#calculate the relative survival curve
#note that the variable year is given in days since 01.01.1960 and that
#age must be multiplied by 365.241 in order to be expressed in days.
rs.surv(Surv(time,cens)~sex+ratetable(age=age*365.241,sex=sex,
year=year),ratetable=slopop,data=rdata)
```

rs.surv.rsadd	<i>Compute a Relative Survival Curve from an additive relative survival model</i>
---------------	---

Description

Computes the predicted relative survival function for an additive relative survival model fitted with maximum likelihood.

Usage

```
rs.surv.rsadd(formula, newdata)
```

Arguments

formula	a rsadd object (Implemented only for models fitted with the codemax.lik (default) option.)
newdata	a data frame with the same variable names as those that appear in the rsadd formula. a predicted curve for each individual in this data frame shall be calculated

Details

Does not work with factor variables - you have to form dummy variables before calling the rsadd function.

Value

a survfit object; see the help on survfit.object for details. The survfit methods are used for print, plot, lines, and points.

References

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." Computer Methods and Programs in Biomedicine, **81**: 272–278

See Also

survfit, survexp

Examples

```
data(slopop)
data(rdata)
#fit a relative survival model
fit <- rsadd(Surv(time,cens)~sex+age+year+ratetable(age=age*365.241,sex=sex,year=year),
  ratetable=slopop,data=rdata,int=c(0:10,15))

#calculate the predicted curve for a male individual, aged 65, diagnosed in 1982
d <- rs.surv.rsadd(fit,newdata=data.frame(sex=1,age=65,year=as.date("1Jul1982")))
#plot the curve (will result in a step function since the baseline is assumed piecewise constant)
plot(d,xscale=365.241)

#calculate the predicted survival curves for each individual in the data set
d <- rs.surv.rsadd(fit,newdata=rdata)
#calculate the average over all predicted survival curves
p.surv <- apply(d$surv,1,mean)
#plot the relative survival curve
plot(d$time/365.241,p.surv,type="b",ylim=c(0,1),xlab="Time",ylab="Relative survival")
```

rs.zph

Behaviour of Covariates in Time for Relative Survival Regression Models

Description

Calculates the scaled partial residuals of a relative survival model (rsadd, rsmul or rstrans)

Usage

```
rs.zph(fit,sc,transform="identity",var.type="sum")
```

Arguments

fit	the result of fitting an additive relative survival model, using the rsadd, rsmul or rstrans function. In the case of multiplicative and transformation models the output is identical to cox.zph function, except no test is performed.
sc	partial residuals calculated by the resid function. This is used to save time if several tests are to be calculated on these residuals and can otherwise be omitted.
transform	a character string specifying how the survival times should be transformed. Possible values are "km", "rank", "identity" and log. The default is "identity".
var.type	a character string specifying the variance used to scale the residuals. Possible values are "each", which estimates the variance for each residual separately, and sum(default), which assumes the same variance for all the residuals.

Value

an object of class `rs.zph`. This function would usually be followed by a plot of the result. The plot gives an estimate of the time-dependent coefficient $\beta(t)$. If the proportional hazards assumption is true, $\beta(t)$ will be a horizontal line.

References

Goodness of fit: Stare J., Pohar Perme M., Henderson R. (2005) "Goodness of fit of relative survival models." *Statistics in Medicine*, **24**: 3911–3925.

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741–1749.

See Also

[rsadd](#), [rsmul](#), [rstrans](#), [resid](#), [cox.zph](#).

Examples

```
data(slopop)
data(rdata)
fit <- rsadd(Surv(time,cens)~sex+ratetable(age=age*365.241,sex=sex,
      year=year),ratetable=slopop,data=rdata,int=5)
rszph <- rs.zph(fit)
plot(rszph)
```

rsadd

Fit an Additive model for Relative Survival

Description

The function fits an additive model to the data. The methods implemented are the maximum likelihood method, the semiparametric method, a glm model with a binomial error and a glm model with a poisson error.

Usage

```
rsadd(formula, data=parent.frame(), ratetable = relsurv::slopop,
      int, na.action, method, init,bwin,centered,cause,control,...)
```

Arguments

<code>formula</code>	a formula object, with the response on the left of a <code>~</code> operator, and the terms on the right. The terms consist of predictor variables separated by the <code>+</code> operator, along with a <code>ratetable</code> term. The <code>ratetable</code> term matches each subject to his/her expected cohort. If the variables are organized and named in the same way as in the population tables, the <code>ratetable</code> term can be omitted. The response must be a survival object as returned by the <code>Surv</code> function. NOTE: The time must be in days, and the same is required for the <code>ratetable</code> variables (the variables used in the population tables), for example age and year (year must be given in the date format, i.e. in number of days since 01.01.1960).
<code>data</code>	a <code>data.frame</code> in which to interpret the variables named in the formula.
<code>ratetable</code>	a table of event rates, organized as a <code>ratetable</code> object, such as <code>slopop</code> .
<code>int</code>	either a single value denoting the number of follow-up years or a vector specifying the intervals (in years) in which the hazard is constant (the times that are bigger than <code>max(int)</code> are censored. If missing, only one interval (from time 0 to maximum observation time) is assumed. The EM method does not need the intervals, only the maximum time can be specified (all times are censored after this time point).
<code>na.action</code>	a missing-data filter function, applied to the <code>model.frame</code> , after any subset argument has been used. Default is <code>options()\$na.action</code> .
<code>method</code>	<code>glm.bin</code> or <code>glm.poi</code> for a glm model, EM for the EM algorithm and <code>max.lik</code> for the maximum likelihood model (default).
<code>init</code>	vector of initial values of the iteration. Default initial value is zero for all variables.
<code>bwin</code>	controls the bandwidth used for smoothing in the EM algorithm. The follow-up time is divided into quartiles and <code>bwin</code> specifies a factor by which the maximum between events time length on each interval is multiplied. The default <code>bwin=-1</code> lets the function find an appropriate value. If <code>bwin=0</code> , no smoothing is applied.
<code>centered</code>	if TRUE, all the variables are centered before fitting and the baseline excess hazard is calculated accordingly. Default is FALSE.
<code>cause</code>	A vector of the same length as the number of cases. 0 for population deaths, 1 for disease specific deaths, 2 (default) for unknown. Can only be used with the EM method.
<code>control</code>	a list of parameters for controlling the fitting process. See the documentation for <code>glm.control</code> for details.
<code>...</code>	other arguments will be passed to <code>glm.control</code> .

Details

NOTE: All times used in the formula argument must be specified in days. This is true for the follow-up time as well as for any variables needed `ratetable` object, like age and year. On the contrary, the `int` argument requires interval specification in years.

The maximum likelihood method and both glm methods assume a fully parametric model with a piecewise constant baseline excess hazard function. The intervals on which the baseline is assumed

constant should be passed via argument `int`. The EM method is semiparametric, i.e. no assumptions are made for the baseline hazard and therefore no intervals need to be specified.

The methods using `glm` are methods for grouped data. The groups are formed according to the covariate values. This should be taken into account when fitting a model. The `glm` method returns life tables for groups specified by the covariates in groups.

The EM method output includes the smoothed baseline excess hazard `lambda0`, the cumulative baseline excess hazard `Lambda0` and times at which they are estimated. The individual probabilities of dying due to the excess risk are returned as `Nie`. The EM method fitting procedure requires some local smoothing of the baseline excess hazard. The default `bwin=-1` value lets the function find an appropriate value for the smoothing band width. While this ensures an unbiased estimate, the procedure time is much longer. As the value found by the function is independent of the covariates in the model, the value can be read from the output (`bwinfac`) and used for refitting different models to the same data to save time.

Value

An object of class `rsadd`. In the case of `method="glm.bin"` and `method="glm.poi"` the class also inherits from `glm` which inherits from the class `lm`. Objects of this class have methods for the functions `print` and `summary`. An object of class `rsadd` is a list containing at least the following components:

<code>data</code>	the data as used in the model, along with the variables defined in the rate table
<code>ratetable</code>	the ratetable used.
<code>int</code>	the maximum time (in years) used. All the events at and after this value are censored.
<code>method</code>	the fitting method that was used.
<code>linear.predictors</code>	the vector of linear predictors, one per subject.

References

- Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272–278
- Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741–1749.
- EM algorithm: Pohar Perme M., Henderson R., Stare, J. (2009) "An approach to estimation in relative survival regression." *Biostatistics*, **10**: 136–146.

See Also

[rstrans](#), [rsmul](#)

Examples

```
data(slopop)
data(rdata)
#fit an additive model
#note that the variable year is given in days since 01.01.1960 and that
```

```
#age must be multiplied by 365.241 in order to be expressed in days.
fit <- rsadd(Surv(time,cens)~sex+as.factor(agegr)+ratetable(age=age*365.241,
  sex=sex,year=year), ratetable=slopop,data=rdata,int=5)

#check the goodness of fit
rs.br(fit)

#use the EM method and plot the smoothed baseline excess hazard
fit <- rsadd(Surv(time,cens)~sex+age+ratetable(age=age*365.241,
  sex=sex,year=year), ratetable=slopop,data=rdata,int=5,method="EM")
sm <- epa(fit)
plot(sm$times,sm$lambda,type="l")
```

rsmul

Fit Andersen et al Multiplicative Regression Model for Relative Survival

Description

Fits the Andersen et al multiplicative regression model in relative survival. An extension of the coxph function using relative survival.

Usage

```
rsmul(formula, data, ratetable = relsurv::slopop, int,na.action,init,
  method,control,...)
```

Arguments

formula	a formula object, with the response on the left of a ~ operator, and the terms on the right. The terms consist of predictor variables separated by the + operator, along with a ratetable term. The ratetable term matches each subject to his/her expected cohort. If the variables are organized and named in the same way as in the population tables, the ratetable term can be omitted. The response must be a survival object as returned by the Surv function. NOTE: The time must be in days, and the same is required for the ratetable variables (the variables used in the population tables), for example age and year (year must be given in the date format, i.e. in number of days since 01.01.1960).
data	a data.frame in which to interpret the variables named in the formula.
ratetable	a table of event rates, such as slopop.
int	the number of follow-up years used for calculating survival(the data are censored after this time-point). If missing, it is set the the maximum observed follow-up time.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
init	vector of initial values of the iteration. Default initial value is zero for all variables.

method	the default method mul assumes hazard to be constant on yearly intervals. Method mul1 uses the ratetable to determine the time points when hazard changes. The mul1 method is therefore more accurate, but at the same time can be more computationally intensive.
control	a list of parameters for controlling the fitting process. See the documentation for coxph.control for details.
...	Other arguments will be passed to coxph.control.

Details

NOTE: All times used in the formula argument must be specified in days. This is true for the follow-up time as well as for any variables needed ratetable object, like age and year. On the contrary, the int argument requires interval specification in years.

Value

an object of class coxph with an additional item:

basehaz Cumulative baseline hazard (population values are seen as offset) at centered values of covariates.

References

Method: Andersen, P.K., Borch-Johnsen, K., Deckert, T., Green, A., Hougaard, P., Keiding, N. and Kreiner, S. (1985) "A Cox regression model for relative mortality and its application to diabetes mellitus survival data.", *Biometrics*, **41**: 921–932.

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741–1749.

See Also

[rsadd](#), [rstrans](#).

Examples

```
data(slopop)
data(rdata)
#fit a multiplicative model
#note that the variable year is given in days since 01.01.1960 and that
#age must be multiplied by 365.241 in order to be expressed in days.
fit <- rsmul(Surv(time,cens)~sex+as.factor(agegr)+ratetable(age=age*365.241,
  sex=sex,year=year),ratetable=slopop,data=rdata)

#check the goodness of fit
rs.br(fit)
```

rstrans

*Fit Cox Proportional Hazards Model in Transformed Time***Description**

The function transforms each person's time to his/her probability of dying at that time according to the ratetable. It then fits the Cox proportional hazards model with the transformed times as a response. It can also be used for calculating the transformed times (no covariates are needed in the formula for that purpose).

Usage

```
rstrans(formula, data, ratetable, int, na.action, init, control, ...)
```

Arguments

formula	a formula object, with the response on the left of a ~ operator, and the terms on the right. The terms consist of predictor variables separated by the + operator, along with a ratetable term. The ratetable term matches each subject to his/her expected cohort. If the variables are organized and named in the same way as in the population tables, the ratetable term can be omitted. The response must be a survival object as returned by the Surv function. NOTE: The time must be in days, and the same is required for the ratetable variables (the variables used in the population tables), for example age and year (year must be given in the date format, i.e. in number of days since 01.01.1960).
data	a data.frame in which to interpret the variables named in the formula.
ratetable	a table of event rates, such as slopop.
int	the number of follow-up years used for calculating survival (the rest is censored). If missing, it is set to the maximum observed follow-up time.
na.action	a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()\$na.action.
init	vector of initial values of the iteration. Default initial value is zero for all variables.
control	a list of parameters for controlling the fitting process. See the documentation for coxph.control for details.
...	other arguments will be passed to coxph.control.

Details

NOTE: All times used in the formula argument must be specified in days. This is true for the follow-up time as well as for any variables needed in the ratetable object, like age and year. On the contrary, the int argument requires interval specification in years.

Value

an object of class `coxph`. See `coxph.object` and `coxph.detail` for details.

`y` an object of class `Surv` containing the transformed times (these times do not depend on covariates).

References

Method: Stare J., Henderson R., Pohar M. (2005) "An individual measure for relative survival." *Journal of the Royal Statistical Society: Series C*, **54** 115–126.

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." *Computer Methods and Programs in Biomedicine*, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." *Computers in biology and medicine*, **37**: 1741–1749.

See Also

[rsmul](#), [invtime](#), [rsadd](#), [survexp](#).

Examples

```
data(slopop)
data(rdata)

#fit a Cox model using the transformed times
#note that the variable year is given in days since 01.01.1960 and that
#age must be multiplied by 365.241 in order to be expressed in days.
fit <- rstrans(Surv(time,cens)~sex+as.factor(agegr)+ratetable(age=age*365.241,
  sex=sex,year=year),ratetable=slopop,data=rdata)

#check the goodness of fit
rs.br(fit)
```

slopop

Census Data Set for the Slovene Population

Description

Census data set for the Slovene population.

Usage

```
data(slopop)
```

Examples

```
data(slopop)
```

survfit.rsadd

*Compute a Predicted Survival Curve***Description**

Computes a predicted survival curve based on the additive model estimated by rsadd function.

Usage

```
## S3 method for class 'rsadd'
survfit(formula, newdata, se.fit = TRUE, conf.int = 0.95, individual = FALSE,
        conf.type = c("log", "log-log", "plain", "none"),...)
```

Arguments

formula	a rsadd object
newdata	a data frame with the same variable names as those that appear in the rsadd formula. The curve(s) produced will be representative of a cohort who's covariates correspond to the values in newdata.
se.fit	a logical value indicating whether standard errors should be computed. Default is TRUE.
conf.int	the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.
individual	a logical value indicating whether the data frame represents different time epochs for only one individual (T), or whether multiple rows indicate multiple individuals (F, the default). If the former only one curve will be produced; if the latter there will be one curve per row in newdata.
conf.type	One of none, plain, log (the default), or log-log. The first option causes confidence intervals not to be generated. The second causes the standard intervals $\text{curve} \pm k * \text{se}(\text{curve})$, where k is determined from conf.int. The log option calculates intervals based on the cumulative hazard or $\log(\text{survival})$. The last option bases intervals on the log hazard or $\log(-\log(\text{survival}))$.
...	Currently not implemented

Details

When predicting the survival curve, the ratetable values for future years will be equal to those of the last given year. The same ratetables will be used for fitting and predicting. To predict a relative survival curve, use `rs.surv.rsadd`.

Value

a survfit object; see the help on survfit.object for details. The survfit methods are used for print, plot, lines, and points.

References

Package: Pohar M., Stare J. (2006) "Relative survival analysis in R." Computer Methods and Programs in Biomedicine, **81**: 272–278.

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." Computers in biology and medicine, **37**: 1741–1749.

See Also

survfit, survexp, [rs.surv](#)

Examples

```
data(slopop)
data(rdata)
fit <- rsadd(Surv(time,cens)~sex+ratetable(age=age*365,sex=sex,
      year=year),ratetable=slopop,data=rdata,method="EM")
survfit.rsadd(fit,newdata=data.frame(sex=1,age=60,year=17000))
```

survsplit

Split a Survival Data Set at Specified Times

Description

Given a survival data set and a set of specified cut times, the function splits each record into multiple records at each cut time. The new data set is be in counting process format, with a start time, stop time, and event status for each record. More general than survSplit as it also works with the data already in the counting process format.

Usage

```
survsplit(data, cut, end, event, start, id = NULL, zero = 0,
  episode = NULL,interval=NULL)
```

Arguments

data	data frame.
cut	vector of timepoints to cut at.
end	character string with name of event time variable.
event	character string with name of censoring indicator.
start	character string with name of start variable (will be created if it does not exist).
id	character string with name of new id variable to create (optional).
zero	If start doesn't already exist, this is the time that the original records start. May be a vector or single value.
episode	character string with name of new episode variable (optional).
interval	this argument is used by max.lik function

Value

New, longer, data frame.

See Also

[survSplit](#).

transrate

Reorganize Data into a Ratetable Object

Description

The function assists in reorganizing certain types of data into a ratetable object.

Usage

```
transrate(men,women,yearlim,int.length=1)
```

Arguments

men	a matrix containing the yearly (conditional) probabilities of one year survival for men. Rows represent age (increasing 1 year per line, starting with 0), the columns represent cohort years (the limits are in yearlim, the increase is in int.length).
women	a matrix containing the yearly (conditional) probabilities of one year survival for women.
yearlim	the first and last cohort year given in the tables.
int.length	the length of intervals in which cohort years are given.

Details

This function only applies for ratetables that are organized by age, sex and year.

Value

An object of class ratetable.

References

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." Computer Methods and Programs in Biomedicine, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." Computers in biology and medicine, **37**: 1741–1749.

See Also

[ratetable](#).

Examples

```
men <- cbind(exp(-365.241*exp(-14.5+.08*(0:100))),exp(-365*exp(-14.7+.085*(0:100))))
women <- cbind(exp(-365.241*exp(-15.5+.085*(0:100))),exp(-365*exp(-15.7+.09*(0:100))))
table <- transrate(men,women,yearlim=c(1980,1990),int.length=10)
```

transrate.hld	<i>Reorganize Data obtained from Human Life-Table Database into a Ratetable Object</i>
---------------	--

Description

The function assists in reorganizing the .txt files obtained from Human Life-Table Database (<http://www.lifetable.de> -> Data by Country) into a ratetable object.

Usage

```
transrate.hld(file,cut.year,race)
```

Arguments

file	a vector of file names which the data are to be read from. Must be in .tex format and in the same format as the files in Human Life-Table Database.
cut.year	a vector of cutpoints for years. Must be specified when the year spans in the files are not consecutive.
race	a vector of race names for the input files.

Details

This function works with any table organised in the format provided by the Human Life-Table Database, but currently only works with TypeLT 1 (i.e. age intervals of length 1). The age must always start with value 0, but can end at different values (when that happens, the last value is carried forward). The rates between the cutpoints are taken to be constant.

Value

An object of class ratetable.

References

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." Computer Methods and Programs in Biomedicine, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." Computers in biology and medicine, **37**: 1741–1749.

See Also

[ratetable](#), [transrate.hmd](#), [joinrate](#), [transrate](#).

Examples

```
## Not run:
finpop <- transrate.hld(c("FIN_1981-85.txt", "FIN_1986-90.txt", "FIN_1991-95.txt"))

## End(Not run)
## Not run:
nzipop <- transrate.hld(c("NZL_1980-82_Non-maori.txt", "NZL_1985-87_Non-maori.txt",
  "NZL_1980-82_Maori.txt", "NZL_1985-87_Maori.txt"),
  cut.year=c(1980,1985),race=rep(c("nonmaori", "maori"),each=2))

## End(Not run)
```

transrate.hmd	<i>Reorganize Data obtained from Human Mortality Database into a Ratetable Object</i>
---------------	---

Description

The function assists in reorganizing the .txt files obtained from Human Mortality Database (<http://www.mortality.org>) into a ratetable object.

Usage

```
transrate.hmd(male, female)
```

Arguments

male	a .txt file, containing the data on males.
female	a .txt file, containing the data on females.

Details

This function works automatically with tables organised in the format provided by the Human Mortality Database. Download Life Tables for Males and Females separately from the column named 1x1 (period life tables, organized by date of death, yearly cutpoints for age as well as calendar year).

If you wish to provide the data in the required format by yourself, note that the only two columns needed are calendar year (Year) and probability of death (qx). Death probabilities must be calculated up to age 110 (in yearly intervals).

Value

An object of class ratetable.

References

Package. Pohar M., Stare J. (2006) "Relative survival analysis in R." Computer Methods and Programs in Biomedicine, **81**: 272–278

Relative survival: Pohar, M., Stare, J. (2007) "Making relative survival analysis relatively easy." Computers in biology and medicine, **37**: 1741–1749.

See Also

[ratetable](#), [transrate.hld](#), [joinrate](#), [transrate](#).

Examples

```
## Not run:  
auspop <- transrate.hmd("mltper_1x1.txt", "fltper_1x1.txt")  
  
## End(Not run)
```

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